

(SHEET 1 OF 16)

[illegible]

Fig. 1

TTT AAG CTC TAT ACA CAT AGT TAC TTG GGA TTT GGA CTG AAA GCT GCA Phe Lys Leu Tyr Thr His Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala 235 240 245	951
AGA CTG GCA ACT CTG GGA GCC CTG GAA GCA AAA GGG ACT GAT GGA CAT Arg Leu Ala Thr Leu Gly Ala Leu Glu Ala Lys Gly Thr Asp Gly His 250 255 260 265	999
ACG TTT CGA AGT GCC TGT TTA CCA AGA TGG TTG GAA GCA GAG TGG ATC Thr Phe Arg Ser Ala Cys Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile 270 275 280	1047
TTT GGG GGT GTG AAA TAC CAG TAT GGT GGT AAC CAA GAA GGG GAG ATG Phe Gly Gly Val Lys Tyr Gln Tyr Gly Gly Asn Gln Glu Gly Glu Met 285 290 295	1095
GGC TTT GAA CCC TGC TAT GCG GAA GTG CTG AGG GTA GTA CAG GGG AAA Gly Phe Glu Pro Cys Tyr Ala Glu Val Leu Arg Val Val Gln Gly Lys 300 305 310	1143
CTT CAC CAG CCA GAA GAA GTC CGA GGA AGC GCC TTC TAC GCT TTC TCT Leu His Gln Pro Glu Glu Val Arg Gly Ser Ala Phe Tyr Ala Phe Ser 315 320 325	1191
TAC TAC TAC GAT CGA GCC GCT GAC ACA CAC TTG ATC GAT TAT GAA AAG Tyr Tyr Tyr Asp Arg Ala Ala Asp Thr His Leu Ile Asp Tyr Glu Lys 330 335 340 345	1239
GGC GGG GTT TTA AAA GTT GAA GAT TTT GAA AGA AAA GCC AGA GAA GTG Gly Gly Val Leu Lys Val Glu Asp Phe Glu Arg Lys Ala Arg Glu Val 350 355 360	1287
TGT GAC AAC TTG GGG AGC TTC TCC TCG GGC AGT CCT TTC CTC TGC ATG Cys Asp Asn Leu Gly Ser Phe Ser Ser Gly Ser Pro Phe Leu Cys Met 365 370 375	1335
GAC CTC ACT TAC ATC ACA GCC CTG TTG AAA GAT GGT TTG GGC TTT GCC Asp Leu Thr Tyr Ile Thr Ala Leu Leu Lys Asp Gly Leu Gly Phe Ala 380 385 390	1383
GAA CGG CAC CCT CTT ACA GCT CAC AAA GAA AGT GAA CAA CAT AGA GAC Glu Arg His Pro Leu Thr Ala His Lys Glu Ser Glu Gln His Arg Asp 395 400 405	1431
TGG TTG GGC CTT GGG GGC CAC CTT TCA CCT GCT CCA GTC TCT GGG CAT Trp Leu Gly Leu Gly Gly His Leu Ser Pro Ala Pro Val Ser Gly His 410 415 420 425	1479
CAC CAG CTG AGG CCA AGC TCC ACC TCT GAA GCC TGC ATT TCT GAA CCA His Gln Leu Arg Pro Ser Ser Thr Ser Glu Ala Cys Ile Ser Glu Pro 430 435 440	1527
GTT TTC TCA CAG GAA GGC GTG GAC TCA GAG ACA TTT TCT GAC CTC TCT Val Phe Ser Gln Glu Gly Val Asp Ser Glu Thr Phe Ser Asp Leu Ser 445 450 455	1575
GGA AAA GCC TGG CCC GAA ACC CGT TAACTGGTTT TATAAGGAGG GAGGGGTTT Gly Lys Ala Trp Pro Glu Thr Arg 460 465	1629

Fig. 1 (cont'd.)

9598-066

(SHEET 3 OF 16)

TAGATGAGTC	TTGCTCTTGA	GCCTAGTGAT	TTGGGGCTTCA	ATGATTTGCA	CATCTAATGT	1689
GAATAGCTCC	TAACCACTTG	GTGGGTGCAT	GGCTGGCACC	AGACTGTAAA	TCTTTTGGGA	1749
TTCTTTGTAC	AGAGTCCTGC	AAAGGAAAAA	AGAGAAAAGG	TTTGGAATC	CATGCTAGAT	1809
TGCGAGTTCA	GAGACAGGTC	CCTGGGGACC	AAAGAACAAT	CTCGTTTCAA	CCCTTGGATG	1869
CCTCATTGCT	TTGAATGGAT	TCATTTTTC	TTATAAGCTG	ATTACTGAA	ATCCCATAAC	1929
CCATCAATGC	TGTTAATTTT	TTTCTTCCTA	CCCTTATTAC	ATTCCCTACC	CTAAAAGCCT	1989
GGGGGAAATA	CCTGGTTTTG	CTTCCCATCT	ATAATTGAGA	AAGAGGGGGG	AAAAGATACT	2049
GTATTAGAAT	TTGTGTGATC	CTGTGGCACA	ATAGATCAAC	CAACCCATT	AAAGCTTAAA	2109
AAAAAAAAAA						2119

Fig. 1 (cont'd.)

9598-066

```

peaNTase 1 ---MELLKLTFFLLFSEKIKSSOYQNNMLTSRPTLKCEIISAVVFDAGSTGSR
potapyrase 1 MLNQNSHFHFIILNMFVLVLESLLSKNVNAQIPRRHILSHSE..HYAVHFDAGSTGSR
mNTase 1 KATSWGAVFMNITACVCSVTFYRQQTWFEGYPLSSMCFYNVSAGTFVGMFDAGSTGSR
yGDPase 1 KTFKHISLTFVNDPEQYLQDGRTEONWPELADAKKSQTSQTCSEHNKVIIDAGSTGSR

peaNTase 57 IHVVEENQNDLTTHICQGVVYHATPOLSSYANPEOAAKSLIPLEQAEVDVVDLQF
potapyrase 59 VHVPASDEKICLIPQNNIPYTHAHPGLSSYAKDPKAAANSLPPLRGACGVVPEQLQS
mNTase 61 IHVVTQVKTACQLPFEGSHIDNNKPCLSATVHOPKOCAEVQELLEVAKDSIPRSHWE
yGDPase 61 YHHKKSQVCT..SPTLLDEKEDMLERGLSSDTPDSVQANSLPPLRVAMNYVPIKAR

peaNTase 117 KTPVRLGATAGLRLLNGDASEKILQSVRDQLSNRSTF.NVQPDVSIHDCQOEGSVLWVA
potapyrase 119 ETPRELGATAGLRLLKGDAAEKILOAVNNYKNQSTF.HSKDQWVTHDCQOEGSVLWVA
mNTase 121 KTFVVLKATAGLRLLPEKAQALLLEVERFKN.SPS.LVPPQGVSIHDCQVETILAWVA
yGDPase 119 CTFVAVKATAGLRLLGDAAKSKILSAVRDELEKDYFSPVVEGQVSIHDCQVETILAWVA

peaNTase 176 VNVALGNLGRKIVTK..TVGVIDLGGGCVQMAVAVSKKAKNAKRYADQDDEYKKVYVKG
potapyrase 178 INYLLGNLGRDQKS..TATIDLGGGCVQMAVAVSNQAKAFQNEGG.HBYVQQKHMS
mNTase 179 VNVLLGQLHGGQGE..TVGTIDLGGGASTQITELPQFER....TLQTPRGVLTSPFPM
yGDPase 179 TNYLLGNLGRGANGPGLPAAVFDLGGGSTQHVKEP...FFPINZKRVGCKKZ..DKVFGD

peaNTase 234 IPVLLVHVSYLEFGREASRAELKLL.....PSPSPNFCLLAGFNGIV
potapyrase 235 KDMVLYVHSYLYIQLAGRAETPKA.....LHMSPNFCALGECGGM
mNTase 232 STEKLYTHSYLGFGLKARLATGGA.....LEAKGT...DQHTFRS
yGDPase 234 ENYTLVQFSLHLCYCLKEGRNKVNSVLVENALKDGKILKGDNTRKGLSSQGLFFKVNKTN

peaNTase 276 TVSGPSPKATVYTSQW....NENKCKNTIRKALKNNYPCPYQNTFCGLWNGGGCN...
potapyrase 277 SHQGYDYKVKPKKQS....SNKRCRRDLTRHALKINAKQRTPECTENGWNGGGCD...
mNTase 270 KCLFRWLEHWFQGV....KYQYGGQEGEGMGFEPCYAEVLRVVQCKDHQPEEVR...
yGDPase 294 EKVYTLSEKPYTIDFIGPDEPSGAQCRRFLTDSEINNKDQCGSPFCSENGVHQPSLVRTRK

peaNTase 328 GKNKCHASSSPZYLPEDTCMVDSSTENFYHNSYDHEHAKEDACALNEEDAKSTYPPDQK
potapyrase 329 GKNKCHASSSPYDIDCAQVGHVDKTPSAAKSIQYINAAVACQNNVADIKSIKPTQDK
mNTase 322 GSA.FYAFSYNYDRADTHLIDYE.KGVYLVVDYERKAREVCHNLQSPSSSG....
yGDPase 354 ESNDLYIFSYVYDRERFLGNPLAFPLNEENDLAREVCAGEAANAVESGAGS...HDEL

peaNTase 388 NYASVYVCHDLIYQVLLVDGFGDPLQKLTGCKEIEYQDAIVEAANPLGNATVKAISALPK
potapyrase 389 NM.FYLCMDLIVEYTLVDGFGCLNKKELTVIXDVOYNNYLVGAANPLGCANIDVNSATTN
mNTase 374 ...FLCMDLITVITALLKDCGLFAERHPLTAKHKSSEQHARDWLGLGHHLSFAPVSGHHQLR
yGDPase 411 ESDSHFCDDLSYQVSLNHTGYDIFLQREHRTCKKIANKE....ICQCLGASVPELKNQNW

peaNTase 448 FPRHMYFV-----
potapyrase 448 FPRHMYFV-----
mNTase 430 PSSTSEACISEPVFSQEGVDSETFSDLSGKAWPETR*
yGDPase 467 KCKHQA-----

```

FIG. 2

ACR II

### ACR III

**ACR IV**

F16.3

9598-066

(HEET 6 OF 16)

GTGGGGTCGT ATCCCGCGGG TGGAGGCCGG GGTGGCGCCG GCCGGGGCGG GGGAGCCCAA	60
AAGACCGGCT GCCGCCTGCT CCCCAGAAAA GGGCACTCGT CTCCGTGGGT GTGGCGGAGC	120
GCGCGGTGCA TGGAAATGGG TATGTGAATG AAAAAAGGTA TCCGTTATGA AACTTCCAGA	180
AAAACGAGCT ACATTTTCA GCAGCCGCAG CACGGTCCTT GGCAACAAG G ATG AGA	237
Met Arg	
1	
AAA ATA TCC AAC CAC GGG AGC CTG CGG GTG GCG AAG GTG GCA TAC CCC	285
Lys Ile Ser Asn His Gly Ser Leu Arg Val Ala Lys Val Ala Tyr Pro	
5 10 15	
CTG GGG CTG TGT GTG GGC GTG TTC ATC TAT GTT GCC TAC ATC AAG TGG	333
Leu Gly Leu Cys Val Gly Val Phe Ile Tyr Val Ala Tyr Ile Lys Trp	
20 25 30	
CAC CGG GCC ACC GCC ACC CAG GCC TTC TTC AGC ATC ACC AGG GCA GCC	381
His Arg Ala Thr Ala Thr Gln Ala Phe Phe Ser Ile Thr Arg Ala Ala	
35 40 45 50	
CCG GGG GCC CGG TGG GGT CAG CAG GCC CAC AGC CCC CTG GGG ACA GCT	429
Pro Gly Ala Arg Trp Gly Gln Gln Ala His Ser Pro Leu Gly Thr Ala	
55 60 65	
GCA GAC GGG CAC GAG GTC TTC TAC GGG ATC ATG TTT GAT GCA GGA AGC	477
Ala Asp Gly His Glu Val Phe Tyr Gly Ile Met Phe Asp Ala Gly Ser	
70 75 80	
ACT GGC ACC CGA GTA CAC GTC TTC CAG TTC ACC CGG CCC CCC AGA GAA	525
Thr Gly Thr Arg Val His Val Phe Gln Phe Thr Arg Pro Pro Arg Glu	
85 90 95	
ACT CCC ACG TTA ACC CAC GAA ACC TTC AAA GCA GTG AAG CCA GGT CTT	573
Thr Pro Thr Leu Thr His Glu Thr Phe Lys Ala Val Lys Pro Gly Leu	
100 105 110	
TCT GCC TAT GCT GAT GAT GTT GAA AAG AGC GCT CAG GGA ATC CGG GAA	621
Ser Ala Tyr Ala Asp Asp Val Glu Lys Ser Ala Gln Gly Ile Arg Glu	
115 120 125 130	
CTA CTG GAT GTT GCT AAA CAG GAC ATT CCG TTC GAC TTC TGG AAG GCC	669
Leu Leu Asp Val Ala Lys Gln Asp Ile Pro Phe Asp Phe Trp Lys Ala	
135 140 145	
ACC CCT CTG GTC CTC AAG GCC ACA GCT GGC TTA CGC CTG TTA CCT GGA	717
Thr Pro Leu Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Gly	
150 155 160	
GAA AAG GCC CAG AAG TTA CTG CAG AAG GTG AAA GAA GTA TTT AAA GCA	765
Glu Lys Ala Gln Lys Leu Leu Gln Lys Val Lys Glu Val Phe Lys Ala	
165 170 175	
TCG CCT TTC CTT GTA GGG GAT GAC TGT GTT TCC ATC ATG AAC GGA ACA	813
Ser Pro Phe Leu Val Gly Asp Asp Cys Val Ser Ile Met Asn Gly Thr	
180 185 190	
GAT GAA GGC GTT TCG GCG TGG ATC ACC ATC AAC TTC CTG ACA GGC AGC	861
Asp Glu Gly Val Ser Ala Trp Ile Thr Ile Asn Phe Leu Thr Gly Ser	
195 200 205 210	
TTG AAA ACT CCA GGA GGG AGC AGC GTG GGC ATG CTG GAC TTG GGC GGA	909
Leu Lys Thr Pro Gly Gly Ser Ser Val Gly Met Leu Asp Leu Gly Gly	
215 220 225	

FIG. 4

9598-066

( SHEET 7 OF 16 )

GGA TCC ACT CAG ATC GCC TTC CTG CCA CGC GTG GAG GGC ACC CTG CAG Gly Ser Thr Gln Ile Ala Phe Leu Pro Arg Val Glu Gly Thr Leu Gln 230 235 240	957
GCC TCC CCA CCC GGC TAC CTG ACG GCA CTG CGG ATG TTT AAC AGG ACC Ala Ser Pro Pro Gly Tyr Leu Thr Ala Leu Arg Met Phe Asn Arg Thr 245 250 255	1005
TAC AAG CTC TAT TCC TAC AGC TAC CTC GGG CTC GGG CTG ATG TCG GCA Tyr Lys Leu Tyr Ser Tyr Ser Tyr Leu Gly Leu Gly Leu Met Ser Ala 260 265 270	1053
CGC CTG GCG ATC CTG GGC GGC GTG GAG GGG CAG CCT GCT AAG GAT GGA Arg Leu Ala Ile Leu Gly Gly Val Glu Gly Gln Pro Ala Lys Asp Gly 275 280 285 290	1101
AAG GAG TTG GTC AGC CCT TGC TTG TCT CCC AGT TTC AAA GGA GAG TGG Lys Glu Leu Val Ser Pro Cys Leu Ser Pro Ser Phe Lys Gly Glu Trp 295 300 305	1149
GAA CAC GCA GAA GTC ACG TAC AGG GTT TCA GGG CAG AAA GCA GCG GCA Glu His Ala Glu Val Thr Tyr Arg Val Ser Gly Gln Lys Ala Ala Ala 310 315 320	1197
AGC CTG CAC GAG CTG TGT GCT GCC AGA GTG TCA GAG GTC CTT CAA AAC Ser Leu His Glu Leu Cys Ala Ala Arg Val Ser Glu Val Leu Gln Asn 325 330 335	1245
AGA GTG CAC AGG ACG GAG GAA GTG AAG CAT GTG GAC TTC TAT GCT TTC Arg Val His Arg Thr Glu Glu Val Lys His Val Asp Phe Tyr Ala Phe 340 345 350	1293
TCC TAC TAT TAC GAC CTT GCA GCT GGT GTG GGC CTC ATA GAT GCG GAG Ser Tyr Tyr Tyr Asp Leu Ala Ala Gly Val Gly Leu Ile Asp Ala Glu 355 360 365 370	1341
AAG GGA GGC AGC CTG GTG GTG GGG GAC TTC GAG ATC GCA GCC AAG TAC Lys Gly Gly Ser Leu Val Val Gly Asp Phe Glu Ile Ala Ala Lys Tyr 375 380 385	1389
GTG TGT CGG ACC CTG GAG ACA CAG CCG CAG AGC AGC CCC TTC TCA TGC Val Cys Arg Thr Leu Glu Thr Gln Pro Gln Ser Ser Pro Phe Ser Cys 390 395 400	1437
ATG GAC CTC ACC TAC GTC AGC CTG CTA CTC CAG GAG TTC GGC TTT CCC Met Asp Leu Thr Tyr Val Ser Leu Leu Leu Gln Glu Phe Gly Phe Pro 405 410 415	1485
AGG AGC AAA GTG CTG AAG CTC ACT CGG AAA ATT GAC AAT GTT GAG ACC Arg Ser Lys Val Leu Lys Leu Thr Arg Lys Ile Asp Asn Val Glu Thr 420 425 430	1533
AGC TGG GCT CTG GGG GCC ATT TTT CAT TAC ATC GAC TCC CTG AAC AGA Ser Trp Ala Leu Gly Ala Ile Phe His Tyr Ile Asp Ser Leu Asn Arg 435 440 445 450	1581
CAG AAG AGT CCA GCC TCA TAGTGGCCGA GCCATCCCTG TCCCCGTCAG CAGTGTCT Gln Lys Ser Pro Ala Ser 455	1637
GTGTGTCTGC ATAAACCCTC CTGTCCTGGA CGTGACTTCA TCCTGAGGAG CCACAGCACA GGCCGTGCTG GCACTTTCTG CACACTGGCT CTGGGACTTG CAGAAGGCCT GGTGCTGCCC TGGCATCAGC CTCTTCCAGT CACATCTGGC CAGAGGGCTG TCTGGACCTG GGCCCTGCTC 1697 1757 1817	

FIG. 4 (cont'd.)

9598-066

( SHEET 8 OF 16 )

AATGCCACCT	GTCTGCCTGG	GCTCCAAGTG	GGCAGGACCA	GGACAGAACC	ACAGGCACAC	1877
ACTGAGGGGG	CAGTGTGGCT	CCCTGCCTGT	CCCATCCCCA	TGCCCCGTCC	GCGGGGCTGT	1937
GGCTGCTGCT	GTGCATGTCC	CTGCGATGGG	AGTCTTGTCT	CCCAGCCTGT	CAGTTTCCTC	1997
CCCAGGGCAG	AGCTCCCCTT	CCTGCAAGAG	TCTGGGAGGC	GGTGCAGGCT	GTCTTGGCTG	2057
CTCTGGGGAA	GCCGAGGGAC	AGCCATAACA	CCCCCGGGAC	AGTAGGTCTG	GGCGGCACCA	2117
CTGGGAACTC	TGGACTTGAG	TGTGTTTGCT	CTTCCTTGGG	TATGAATGTG	TGAGTTCACC	2177
CAGAGGCCTG	CTCTCCTCAC	ACATTGTGTG	GTTTGGGGTT	AATGATGGAG	GGAGACACCT	2237
CTTCATAGAC	GGCAGGTGCC	CACCTTTCAG	GGAGTCTCCC	AGCATGGGCG	GATGCCGGGC	2297
ATGAGCTGCT	GTAAACTATT	TGTGGCTGTG	CTGCTTGAGT	GACGTCTCTG	TCGTGTGGGT	2357
GCCAAGTGCT	TGTGTAGAAA	CTGTGTTCTG	AGCCCCCTTT	TCTGGACACC	AACTGTGTCC	2417
TGTGAATGTA	TCGCTACTGT	GAGCTGTTC	CGCCTAGCCA	GGGCCATGTC	TTAGGTGCAG	2477
CTGTGCCACG	GGTCAGCTGA	GCCACAGTCC	CAGAACCAAG	CTCTCGGTGT	CTCGGGCCAC	2537
CATCCGCCCC	CCTCGGGCTG	ACCCACCTC	CTCCATGGAC	AGTGTGAGCC	CCGGGCCGTG	2597
CATCCTGCTC	AGTGTGGCGT	CAGTGTGCGG	GCTGAGCCCC	TTGAGCTGCT	TCAGTGAATG	2657
TACAGTGCCC	GGCACGAGCT	GAACCTCATG	TGTTCCACTC	CCAATAAAAG	GTGACAGGG	2717
GCTTCTCCTT	CAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAA		2762

Fig. 4 (cont'd)

9598-066



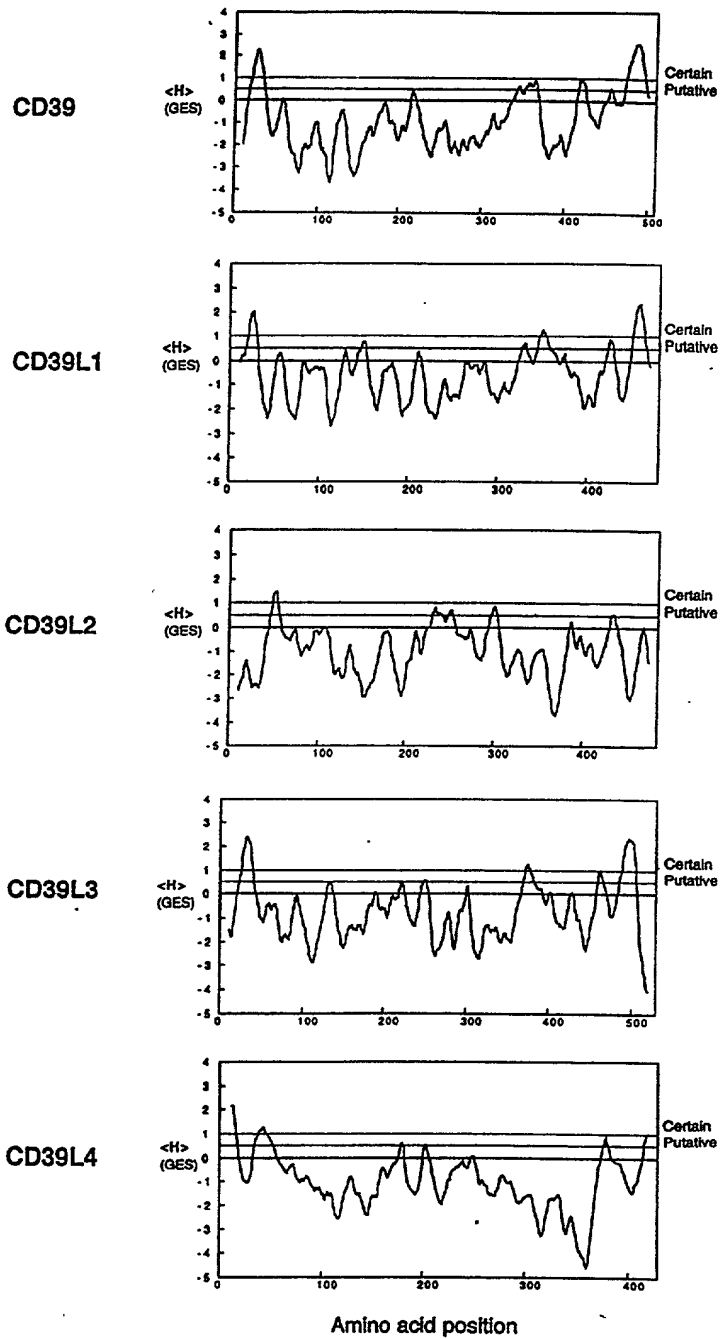


FIG. 5

9598-066

SHEET 10 OF 16 )

ACCCACGCGT CTGGCCGCGG GCCGCCTCTG CGGCAGCGCT AGTCGCCTTC TCCGAATCGG	60
CTCCGCACAG CTAGGAGAAA AG ATG TTC ACT GTG CTG ACC CGC CAA CCA TGT	112
Met Phe Thr Val Leu Thr Arg Gln Pro Cys	
1 5 10	
GAG CAA GCA GGC CTC AAG GCC CTC TAC CGA ACT CCA ACC ATC ATT GCC	160
Glu Gln Ala Gly Leu Lys Ala Leu Tyr Arg Thr Pro Thr Ile Ile Ala	
15 20 25	
TTG GTG GTC TTG CTT GTG AGT ATT GTG GTA CTT GTG AGT ATC ACT GTC	208
Leu Val Val Leu Leu Val Ser Ile Val Val Leu Val Ser Ile Thr Val	
30 35 40	
ATC CAG ATC CAC AAG CAA GAG GTC CTC CCT CCA GGA CTG AAG TAT GGT	256
Ile Gln Ile His Lys Gln Glu Val Leu Pro Pro Gly Leu Lys Tyr Gly	
45 50 55	
ATT GTG CTG GAT GCC GGG TCT TCA AGA ACC ACA GTC TAC GTG TAT CAA	304
Ile Val Leu Asp Ala Gly Ser Ser Arg Thr Thr Val Tyr Val Tyr Gln	
60 65 70	
TGG CCA GCA GAA AAA GAG AAT AAT ACC GGA GTG GTC AGT CAA ACC TTC	352
Trp Pro Ala Glu Lys Glu Asn Asn Thr Gly Val Val Ser Gln Thr Phe	
75 80 85 90	
AAA TGT AGT GTG AAA GGC TCT GGA ATC TCC AGC TAT GGA AAT AAC CCC	400
Lys Cys Ser Val Lys Gly Ser Gly Ile Ser Ser Tyr Gly Asn Asn Pro	
95 100 105	
CAA GAT GTC CCC AGA GCC TTT GAG GAG TGT ATG CAA AAA GTC AAG GGG	448
Gln Asp Val Pro Arg Ala Phe Glu Glu Cys Met Gln Lys Val Lys Gly	
110 115 120	
CAG GTT CCA TCC CAC CTC CAC GGA TCC ACC CCC ATT CAC CTG GGA GCC	496
Gln Val Pro Ser His Leu His Gly Ser Thr Pro Ile His Leu Gly Ala	
125 130 135	
ACG GCT GGG ATG CGC TTG CTG AGG TTG CAA AAT GAA ACA GCA GCT AAT	544
Thr Ala Gly Met Arg Leu Leu Arg Leu Gln Asn Glu Thr Ala Ala Asn	
140 145 150	
GAA GTC CTT GAA AGC ATC CAA AGC TAC TTC AAG TCC CAG CCC TTT GAC	592
Glu Val Leu Glu Ser Ile Gln Ser Tyr Phe Lys Ser Gln Pro Phe Asp	
155 160 165 170	
TTT AGG GGT GCT CAA ATC ATT TCT GGG CAA GAA GAA GGG GTA TAT GGA	640
Phe Arg Gly Ala Gln Ile Ile Ser Gly Gln Glu Glu Gly Val Tyr Gly	
175 180 185	
TGG ATT ACA GCC AAC TAT TTA ATG GGA AAT TTC CTG GAG AAG AAC CTG	688
Trp Ile Thr Ala Asn Tyr Leu Met Gly Asn Phe Leu Glu Lys Asn Leu	
190 195 200	
TGG CAC ATG TGG GTG CAC CCG CAT GGA GTG GAA ACC ACG GGT GCC CTG	736
Trp His Met Trp Val His Pro His Gly Val Glu Thr Thr Gly Ala Leu	
205 210 215	
GAC TTA GGT GGT GCC TCC ACC CAA ATA TCC TTC GTG GCA GGA GAG AAG	784
Asp Leu Gly Gly Ala Ser Thr Gln Ile Ser Phe Val Ala Gly Glu Lys	
220 225 230	

Fig. 6

ATG GAT CTG AAC ACC AGC GAC ATC ATG CAG GTG TCC CTG TAT GGC TAC Met Asp Leu Asn Thr Ser Asp Ile Met Gln Val Ser Leu Tyr Gly Tyr 235 240 245 250	832
GTA TAC ACG CTC TAC ACA CAC AGC TTC CAG TGC TAT GGC CGG AAT GAG Val Tyr Thr Leu Tyr Thr His Ser Phe Gln Cys Tyr Gly Arg Asn Glu 255 260 265	880
GCT GAG AAG AAG TTT CTG GCA ATG CTC CTG CAG AAT TCT CCT ACC AAA Ala Glu Lys Lys Phe Leu Ala Met Leu Leu Gln Asn Ser Pro Thr Lys 270 275 280	928
AAC CAT CTC ACC AAT CCC TGT TAC CCT CGG GAT TAT AGC ATC AGC TTC Asn His Leu Thr Asn Pro Cys Tyr Pro Arg Asp Tyr Ser Ile Ser Phe 285 290 295	976
ACC ATG GGC CAT GTA TTT GAT AGC CTG TGC ACT GTG GAC CAG AGG CCA Thr Met Gly His Val Phe Asp Ser Leu Cys Thr Val Asp Gln Arg Pro 300 305 310	1024
GAA AGT TAT AAC CCC AAT GAT GTC ATC ACT TTT GAA GGA ACT GGG GAC Glu Ser Tyr Asn Pro Asn Asp Val Ile Thr Phe Glu Gly Thr Gly Asp 315 320 325 330	1072
CCA TCT CTG TGT AAG GAG AAG GTG GCT TCC ATA TTT GAC TTC AAA GCT Pro Ser Leu Cys Lys Glu Lys Val Ala Ser Ile Phe Asp Phe Lys Ala 335 340 345	1120
TGC CAT GAT CAA GAA ACC TGT TCT TTT GAT GGG GTT TAT CAG CCA AAG Cys His Asp Gln Glu Thr Cys Ser Phe Asp Gly Val Tyr Gln Pro Lys 350 355 360	1168
ATT AAA GGG CCA TTT GTG GCT TTT GCA GGA TTC TAC TAC ACA GCC AGT Ile Lys Gly Pro Phe Val Ala Phe Ala Gly Phe Tyr Tyr Thr Ala Ser 365 370 375	1216
GCT TTA AAT CTT TCA GGT AGC TTT TCC CTG GAC ACC TTC AAC TCC AGC Ala Leu Asn Leu Ser Gly Ser Phe Ser Leu Asp Thr Phe Asn Ser Ser 380 385 390	1264
ACC TGG AAT TTC TGC TCA CAG AAT TGG AGT CAG CTC CCA CTG CTG CTC Thr Trp Asn Phe Cys Ser Gln Asn Trp Ser Gln Leu Pro Leu Leu Leu 395 400 405 410	1312
CCC AAA TTT GAT GAG GTA TAT GCC CGC TCT TAC TGC TTC TCA GCC AAC Pro Lys Phe Asp Glu Val Tyr Ala Arg Ser Tyr Cys Phe Ser Ala Asn 415 420 425	1360
TAC ATC TAC CAC TTG TTT GTG AAC GGT TAC AAA TTC ACA GAG GAG ACT Tyr Ile Tyr His Leu Phe Val Asn Gly Tyr Lys Phe Thr Glu Glu Thr 430 435 440	1408
TGG CCC CAA ATA CAC TTT GAA AAA GAA GTG GGG AAT AGC AGC ATA GCC Trp Pro Gln Ile His Phe Glu Lys Glu Val Gly Asn Ser Ser Ile Ala 445 450 455	1456
TGG TCT CTT GGC TAC ATG CTC AGC CTG ACC AAC CAG ATC CCA GCT GAA Trp Ser Leu Gly Tyr Met Leu Ser Leu Thr Asn Gln Ile Pro Ala Glu 460 465 470	1504
AGC CCT CTG ATC CGT CTG CCC ATA GAA CCA CCT GTC TTT GTG GGC ACC Ser Pro Leu Ile Arg Leu Pro Ile Glu Pro Pro Val Phe Val Gly Thr 475 480 485 490	1552

FIG. 6 (cont'd.)

9598-066

(SHEET 12 OF 16)

CTC GCT TTC TTC ACA GTG GCA GCC TTG CTG TGT CTG GCA TTT CTT GCA 1600  
 Leu Ala Phe Phe Thr Val Ala Ala Leu Leu Cys Leu Ala Phe Leu Ala  
 495 500 505

TAC CTG TGT TCA GCA ACC AGA AGA AAG AGG CAC TCC GAG CAT GCC TTT 1648  
 Tyr Leu Cys Ser Ala Thr Arg Arg Lys Arg His Ser Glu His Ala Phe  
 510 515 520

GAC CAT GCA GTG GAT TCT GAC TGAGCCTTCA AAGCAGCTCC TGGAGTCCAA TGGC 1703  
 Asp His Ala Val Asp Ser Asp  
 525

TGCTTAGAGT CAGCCTGGGT GGCACCAGGC AATGCAGGTG AAGTGGCTGC CTTCAGGAAA 1763  
 TACAACCTAAC TAAAATCAAA CACCTAGGTC ACGTGCCTCT CAAATACTGA TTTCTGCCAC 1823  
 AGCACCTCTT GAGGCATCCC TTGGCTATTG TGTGCATATT GTTCTTCAGA GACCTCACTA 1883  
 CCCACATGCT GATCTATTGG GGAACAGAGA AGAGACAGGC CACTAAGGTC AGGCTCTTTA 1943  
 TATTAAGTTC CCCAGAGGAA GAGTAAGTTG AGAAGGTATC AGTTTAATGT TGAAGAATTG 2003  
 ACCTCAGGGC TCAGTTTCCA TTTCCCTCCC TCAGTATTCT TCCTGGCAAG ATACCCATTA 2063  
 AGCATTTCGC CAATCAGAAT CTCATTTTAT AGTTTTTCCC ATTGGTCTTT AACTAAGACT 2123  
 TTCTTGTAGC AATCTCGTAA GCAGTGAACC CCCTCAGATC AGTAGAATAT AGTATCTGGG 2183  
 GGAGAAGACT TACTTCCTTC AGGGCAGCAG CCACAGCCAG GCTTCTGTCA TACAGGTAGA 2243  
 TCCCGAAGCA CAGAGACATA AAAAAGGTCT CCCAGAAAAC TATAGACCAT TCTCCAAGTG 2303  
 GAATTCCAC TTAGGGCTCT GGTCACTAGA TTGCAACCTG TGTGTTTGTG ATCATCTCTCA 2363  
 TCTCACCATT GTATTGCTAT GCCCTCCCAT AAAACACAT TGATCCCTAG CAAGATTATT 2423  
 GCATTCCAGA TTTTACTGCC TTTGCTAGGC TTTTGCTTAG CAAAGGGCTG ACTTTCCATT 2483  
 GTTATCATGG TGTATATATT TTTGTCACCA TTCCCAAG TATACTTGAT GTTGTCATAG 2543  
 AACGAACATC CTACTCTATG ATTTACTAAC CAATTACTTT CCCAGATCAT AGACCTCTCT 2603  
 GCATAGTAGT CATAGGTCTT GACTTTGGGG AAAGAAAAGG AAGCTGCAGG AATATTTATC 2663  
 TCCAAAGTCG AATGAGAAAG AACTCCAGCA AATCCAATGG CTACAAACTA AAAATCAGCA 2723  
 TTATTTTATA TTGCTGTTTC TTAGCTGAAT ATGGAATAAA GAACTATTAT TTTATTTTGA 2783  
 AAAAAAAAAA AAAA 2797

Fig. 6 (cont.d.)

[illegible][illegible]

FIG. 7

ACA CAT AGT TAC TTG GGA TTT GGA TTG AAA GCT GCA AGA CTA GCA ACC	1008
Thr His Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr	
240 245 250	
CTG GGA GCC CTG GAG ACA GAA GGG ACT GAT GGG CAC ACT TTC CGG AGT	1056
Leu Gly Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser	
255 260 265 270	
GCC TGT TTA CCG AGA TGG TTG GAA GCA GAG TGG ATC TTT GGG GGT GTG	1104
Ala Cys Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val	
275 280 285	
AAA TAC CAG TAT GGT GGC AAC CAA GAA GGG GAG GTG GGC TTT GAG CCC	1152
Lys Tyr Gln Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro	
290 295 300	
TGC TAT GCC GAA GTG CTG AGG GTG GTA CGA GGA AAA CTT CAC CAG CCA	1200
Cys Tyr Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro	
305 310 315	
GAG GAG GTC CAG AGA GGT TCC TTC TAT GCT TTC TCT TAC TAT TAT GAC	1248
Glu Glu Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp	
320 325 330	
CGA GCT GTT GAC ACA GAC ATG ATT GAT TAT GAA AAG GGG GGT ATT TTA	1296
Arg Ala Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Gly Ile Leu	
335 340 345 350	
AAA GTT GAA GAT TTT GAA AGA AAA GCC AGG GAA GTG TGT GAT AAC TTG	1344
Lys Val Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu	
355 360 365	
GAA AAC TTC ACC TCA GGC AGT CCT TTC CTG TGC ATG GAT CTC AGC TAC	1392
Glu Asn Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr	
370 375 380	
ATC ACA GCC CTG TTA AAG GAT GGC TTT GGC TTT GCA GAC AGC ACA GTC	1440
Ile Thr Ala Leu Leu Lys Asp Gly Phe Gly Phe Ala Asp Ser Thr Val	
385 390 395	
TTA CAG CTC ACA AAG AAA GTG AAC AAC ATA GAG ACG GGC TGG GCC TTG	1488
Leu Gln Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu	
400 405 410	
GGG GCC ACC TTT CAC CTG TTG CAG TCT CTG GGC ATC TCC CAT TGAGGCCAC	1539
Gly Ala Thr Phe His Leu Leu Gln Ser Leu Gly Ile Ser His	
415 420 425	
GTACTTCCTT GGAGACCTGC ATTTGCCAAC ACCTTTTAA GGGGAGGAGA GAGCACTTAG	1599
TTTCTGAACT AGTCTGGGAC ATCCTGGACT TGAGCCTAGA GATTAGGTT TAATTAATTT	1659
TACACATCTA ATGTGAACTG CTGCCTAACC ACTCAAGAGT ACACAGCTGG CACCAGAGCA	1719
TCACAGAGAG CCCTGTGAGC CAAAAAGTAT AGTTTTGGAA CTTAACCTTG GAGTGAGAGC	1779
CCAGGGACAG GTCCCTGGAA ACCAAAGAAA AATCGCATT CAACCCCTTG AGTGCCTCAT	1839
TCCACTGAAT ATTTAAATTT TCCTCTTAAA TGGTAAACTG ACTTATTGCA ATCCCAAGAC	1899
CCATCAATAT CAGTATTTTT TTCCTCCCTA TACAGTGCCC TGCCACCCCT TATCTGCACC	1959
CACCTCCCTT GAAAAAGAGA GAAAAAATA AAAAAAATA	1998

Fig. 7 (cont'd.)

F. G. 8

peaGDP 1 -----  
 potapyrase 1 -----  
 CD39L2 1 MKKGIRYRTSRKTSYIFQOPQHGPNQTRM K K H H G S L V A V Y T P L G L C V G V F Y Y M K H M  
 CD39L4 1 -----  
 dNTPase 1 -----  
 yGDPase 1 -----

## ACR I

peaGDP 2 E L K L I T F F S S P I S S O Y L S N H L T S R K I F E E I S S Y A F D A G S T G S R H V Y  
 potapyrase 6 S H P I F I L F L V L E L S L L S K N V N A O I F U R R E L L S H S E . . . Y A F D A G S T G S R V H V  
 CD39L2 61 K W H R A T A T Q A Y S T R P G A R N G O A H S P L A A G H E V Y I I F D A G S T G R V H V  
 CD39L4 7 T F F I A V H C V C S A V H R N Q O T F E G H L S S C F N V S A S T L Y I I F D A G S T G R H V Y  
 dNTPase 37 K I S F C I I S V I L L F V F G F V S E N A S P L A R L S K F G Y S K V A A I F D A G S T G S R V L A V  
 yGDPase 5 D S H P E N D E F G Y L Q D S K E O N Y E L A D A K S Q S Q T C S E E H Y V I I F D A G S T G S R V H V

## ACR II

peaGDP 61 E F N O M D L L E I S K G E Y K T P G L S S Y A P E Q A A K S L I P L L Q A E D V V P D L Q E K T P V  
 potapyrase 63 F F K I L G L L E I S N N E Y P M A T E P G L S S Y A D P K A A A N S L P L L D C A G V V P D L Q E S T P P  
 CD39L2 119 Q E T E P P R R T P T T H E T K A V K P G L S Y A D D V E K A G R E L L D V A R Q D P E G F A L A P E  
 CD39L4 66 T F V K P G Q L P I L E C E V P D V K P G L S Y V D Q P F O A E T G L L V A R D S P S H E K T P V  
 dNTPase 96 K F N R S F I D N K L V Y E L E K E R K P G L S S A D E A V H S K L L I D E A A F P E R H S S T P P  
 yGDPase 65 K F N . . . T C S E T L L D E K F E M P G L S S D T S V G A A N S L P L L K V A A Y V E T K A R S C T P V

## ACR II

## ACR III

peaGDP 121 R E C A T A G L R L L N G D A E K I L O V R D L S N S T F N V P D A V S I D G T C E G S Y L V T V N N A  
 potapyrase 123 E C C A T A G L R L L S D A E K I L O A V R L V K N O S T F H E K D O W I D G T C E G S Y M M A I N N Y L  
 CD39L2 178 V L K A T A G L R L L F G K A K L O K V F E H A S P F E V C D E C Y S I E C D E G V S A R T N L  
 CD39L4 126 V L K A T A G L R L L P E H K A K L L I V F E I K S P F E V E K G V S I M E C D E G L A W T V N L  
 dNTPase 156 V L K A T A G L R L L P K A E H I L A V R D L E A K S E F E V M D A V E I I N C T D E G L E W T V N L  
 yGDPase 123 A K R A T A G L R L L O D A R S K I L S A V R D H L E K D T E F F A V G D V S I N G D E G V A R A T T N Y L

## ACR IV

peaGDP 180 L G N L G R E Y T K . . . T V G V D L G G G S V C A A V S K K T A K N A P I W A D G D P Y K K V V E K G I P Y R  
 potapyrase 182 L G N L G R D Y K S . . . T F T D L G G G S V C A A V S E Q F A K A P O M E D G S P Y Q K H M S D Y N  
 CD39L2 236 T G S L K T P G G S . . . T V G D L D L G G S T C I A F L P R V E G . . . . . T E A S P F G Y L T A R F E N S T Y K  
 CD39L4 184 T G S L K E R Q E . . . T V G T L D L G G S T C I F L Q E E K . . . . . T E Q T P R G Y L T S F E F N S T Y K  
 dNTPase 214 L G N S K T M O H . . . A . . . D L G G G S T C I F A P D P D . . . . . Q V P V Y K . . . E V E V T S S K I N  
 yGDPase 183 L G N E G A N G K L P A L V F D L G G G S T C I V E F E F P I N E K M V . . . . . Q E H K T K K F G E N Y T

peaGDP 238 L Y V H S Y L E F G R E A R A H L N L T P H S . . . . . M P C L E A G F N G . . . . . Y  
 potapyrase 239 L Y V H S Y L E G O L A R A E I F R S R M S . . . . . M P C A L E G C C F . . . . . Y  
 CD39L2 289 L Y T S Y L G L G L E A R L A I L G E C E E R D G N E L Y . . . . . S P C L G S P F K . . . . . E  
 CD39L4 237 L Y T S Y L G F G L A A R L A T C A L E T S . . . . . T P G E T F E . . . . . S A C L F W L E . . . . . E  
 dNTPase 264 L Y T S Y L G L G L A A R A F . . . . . T G Y K N D T F E . . . . . S V C M E I I A H . . . . . E  
 yGDPase 238 L Y Q T S B L G G L K I P N K I M S V I V E N A L K D C K L G D N T K T H O L S E C L P K A V N T M E K T

peaGDP 276 T V G G L E K A Y T I N G . . . E H N K C N T I R A L K L N Y C P I O N C T F G C W N G G . . . . . S G M G O H N  
 potapyrase 277 E Y G G V D Y K V K P K S . . . S E W K S R R L T R A L K N A C S E E E C T F N G V W N G C . . . . . S C D G O H N  
 CD39L2 335 E H E V T Y K V S G K A S L E E L C A R . . . . . S E . . . . . S O H R V . . . . . H R T . . . . . E E V K E V  
 CD39L4 282 I L G G V K Y Q C Q E C E V C E E P I A E . . . . . V L E . . . . . V R G K L . . . . . H Q F . . . . . E E V Q R G S  
 dNTPase 308 E Y G V Q P H V S K E K S S A E O P I V D F D A C L E L . . . . . U K S V M P L K F P . . . . . F T A D H A  
 yGDPase 298 L E S K I T T D F I G P D H P S G A Q C R F L D E H N K K Q C S P F C S P H C V H P S L Y R T F K S H N

peaGDP 332 F A S S S F I L P L D T G H V D A G E P N T L E P V D I E T R A K E A C A L H P E A R S M P F L K N V S  
 potapyrase 333 H E A S S F Y D I A Q V C V D K P S S C A E P I O N L M A R V A C T N V D I K S I A P K T O P N I P  
 CD39L2 379 F V A F S Y Y D L A A C V S D A E K G G S U V V C D E I A A K T V C R T . . . . . L E T P S S P  
 CD39L4 326 F V A F S Y Y D R A V O T D D Y E K G G I L K V E D E K A E V C D N . . . . . L E S T T S C S P  
 dNTPase 360 F A F S Y . . . F R A T E G V E P L A S G E T T V E A W R K A C E I C A I . . . . . P M O E . . . . . C P  
 yGDPase 358 I Y T P S Y F Y D R A F L S P L F L L E N E N D H A R I V C R E E W N E V E N C H A G D . . . . . D E L E S D S

peaGDP 392 F L C H D L I Y O I V G L V D G F G L E F L O K I T S G K I I Y O A V E A A W P L C N A V E A S L P K F E R R  
 potapyrase 393 F L C H D L I Y I T G L Y D G F G L H E R E R T I I D H O I K N I V G A A E S L C C A I D E S S T N K I R  
 CD39L2 428 F E C H D L I Y V S L L Q L P G F P R S V K L T R I D N . . . . . V E E W A L G A I F H I D S I N H O S P  
 CD39L4 375 F L C H D L I Y I L L K D G F G F A D S T V Q L T K E N . . . . . E E E W A L G A I F H I D S I N H O S P  
 dNTPase 406 E M C P D L I L S T L I R G R L D C K K I L Y K I D G . . . . . H E I E W A L G A I F H I D S I N H O S P  
 yGDPase 415 H F C D L S Q V E L L E T S G D T P L Q E E T O R K I A N N . . . . . E I E W A L G A I F H I D S I N H O S P

peaGDP 452 M Y F V  
 potapyrase 452 A S H  
 CD39L2 483 A S V  
 CD39L4 429 ----  
 dNTPase 462 ----  
 yGDPase 471 Q S H

Fig. 9